0500 #4
D7
01-23-01

OIPE

ENTERED

RAW SEQUENCE LISTING   DATE: 08/17/2000
PATENT APPLICATION: US/09/632,098   TIME: 10:48:16

Input Set : A:\9939.SEQ.txt
Output Set: N:\CRF3\08162000\I632098.raw

```
     4 <110> APPLICANT: Sheppard, Paul O.
     5         Baindur, Nand
     6         Bishop, Paul D.
     8 <120> TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
    10 <130> FILE REFERENCE: 99-39
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/632,098
C--> 12 <141> CURRENT FILING DATE: 2000-08-02
    12 <160> NUMBER OF SEQ ID NOS: 26
    14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    16 <210> SEQ ID NO: 1
    17 <211> LENGTH: 3431
    18 <212> TYPE: DNA
    19 <213> ORGANISM: Homo sapiens
    21 <220> FEATURE:
    22 <221> NAME/KEY: CDS
    23 <222> LOCATION: (37)...(2442)
    25 <400> SEQUENCE: 1
    26 gcgagccgct gcctagaggc cgaggagctc acagct atg ggc tgg agg ccc cgg        54
    27                                         Met Gly Trp Arg Pro Arg
    28                                          1               5
    30 aga gct cgg ggg acc ccg ttg ctg ctg ctg cta cta ctg ctg ctg ctc      102
    31 Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
    32            10              15                  20
    34 tgg cca gtg cca ggc gcc ggg gtg ctt caa gga cat atc cct ggg cag      150
    35 Trp Pro Val Pro Gly Ala Gly Val Leu Gln Gly His Ile Pro Gly Gln
    36            25                  30                  35
    38 cca gtc acc ccg cac tgg gtc ctg gat gga caa ccc tgg cgc acc gtc      198
    39 Pro Val Thr Pro His Trp Val Leu Asp Gly Gln Pro Trp Arg Thr Val
    40            40                  45                  50
    43 agc ctg gag gag ccg gtc tcg aag cca gac atg ggg ctg gtg gcc ctg      246
    44 Ser Leu Glu Glu Pro Val Ser Lys Pro Asp Met Gly Leu Val Ala Leu
    45    55                  60                  65                  70
    47 gag gct gaa ggc cag gag ctc ctg ctt gag ctg gag aag aac cac agg      294
    48 Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu Leu Glu Lys Asn His Arg
    49            75                  80                  85
    51 ctg ctg gcc cca gga tac ata gaa acc cac tac ggc cca gat ggg cag      342
    52 Leu Leu Ala Pro Gly Tyr Ile Glu Thr His Tyr Gly Pro Asp Gly Gln
    53            90                  95                 100
    55 cca gtg gtg ctg gcc ccc aac cac acg gat cat tgc cac tac caa ggg      390
    56 Pro Val Val Leu Ala Pro Asn His Thr Asp His Cys His Tyr Gln Gly
    57           105                 110                 115
    59 cga gta agg ggc ttc ccc gac tcc tgg gta gtc ctc tgc acc tgc tct      438
    60 Arg Val Arg Gly Phe Pro Asp Ser Trp Val Val Leu Cys Thr Cys Ser
    61           120                 125                 130
    63 ggg atg agt ggc ctg atc acc ctc agc agg aat gcc agc tat tat ctg      486
    64 Gly Met Ser Gly Leu Ile Thr Leu Ser Arg Asn Ala Ser Tyr Tyr Leu
    65 135                 140                 145                 150
```

```
67  cgt ccc tgg cca ccc cgg ggc tcc aag gac ttc tca acc cac gag atc      534
68  Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp Phe Ser Thr His Glu Ile
69           155                 160                 165
71  ttt cgg atg gag cag ctg ctc acc tgg aaa gga acc tgt ggc cac agg      582
72  Phe Arg Met Glu Gln Leu Leu Thr Trp Lys Gly Thr Cys Gly His Arg
73           170                 175                 180
75  gat cct ggg aac aaa gcg ggc atg acc agc ctt cct ggt ggt ccc cag      630
76  Asp Pro Gly Asn Lys Ala Gly Met Thr Ser Leu Pro Gly Gly Pro Gln
77           185                 190                 195
79  agc agg ggc agg cga gaa gcg cgc agg acc cgg aag tac ctg gaa ctg      678
80  Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr Arg Lys Tyr Leu Glu Leu
81       200                 205                 210
83  tac att gtg gca gac cac acc ctg ttc ttg act cgg cac cga aac ttg      726
84  Tyr Ile Val Ala Asp His Thr Leu Phe Leu Thr Arg His Arg Asn Leu
85  215                 220                 225                 230
87  aac cac acc aaa cag cgt ctc ctg gaa gtc gcc aac tac gtg gac cag      774
88  Asn His Thr Lys Gln Arg Leu Leu Glu Val Ala Asn Tyr Val Asp Gln
89               235                 240                 245
91  ctt ctc agg act ctg gac att cag gtg gcg ctg acc ggc ctg gag gtg      822
92  Leu Leu Arg Thr Leu Asp Ile Gln Val Ala Leu Thr Gly Leu Glu Val
93               250                 255                 260
95  tgg acc gag cgg gac cgc agc cgc gtc acg cag gac gcc aac gcc acg      870
96  Trp Thr Glu Arg Asp Arg Ser Arg Val Thr Gln Asp Ala Asn Ala Thr
97           265                 270                 275
99  ctc tgg gcc ttc ctg cag tgg cgc cgg ggg ctg tgg gcg cag cgg ccc      918
100 Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly Leu Trp Ala Gln Arg Pro
101      280                 285                 290
103 cac gac tcc gcg cag ctg ctc acg ggc cgc gcc ttc cag ggc gcc aca      966
104 His Asp Ser Ala Gln Leu Leu Thr Gly Arg Ala Phe Gln Gly Ala Thr
105 295                 300                 305                 310
107 gtg ggc ctg gcg ccc gtc gag ggc atg tgc cgc gcc gag agc tcg gga      1014
108 Val Gly Leu Ala Pro Val Glu Gly Met Cys Arg Ala Glu Ser Ser Gly
109              315                 320                 325
111 ggc gtg agc acg gac cac tcg gag ctc ccc atc ggc gcc gca gcc acc      1062
112 Gly Val Ser Thr Asp His Ser Glu Leu Pro Ile Gly Ala Ala Ala Thr
113          330                 335                 340
115 atg gcc cat gag atc ggc cac agc ctc ggc ctc agc cac gac ccc gac      1110
116 Met Ala His Glu Ile Gly His Ser Leu Gly Leu Ser His Asp Pro Asp
117          345                 350                 355
119 ggc tgc tgc gtg gag gct gcg gcc gag tcc gga ggc tgc gtc atg gct      1158
120 Gly Cys Cys Val Glu Ala Ala Ala Glu Ser Gly Gly Cys Val Met Ala
121      360                 365                 370
123 gcg gcc acc ggg cac ccg ttt ccg cgc gtg ttc agc gcc tgc agc cgc      1206
124 Ala Ala Thr Gly His Pro Phe Pro Arg Val Phe Ser Ala Cys Ser Arg
125 375                 380                 385                 390
128 cgc cag ctg cgc gcc ttc ttc cgc aag ggg ggc ggc gct tgc ctc tcc      1254
129 Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly Gly Gly Ala Cys Leu Ser
130              395                 400                 405
132 aat gcc ccg gac ccc gga ctc ccg gtg ccg ccg gcg ctc tgc ggg aac      1302
```

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```
133  Asn Ala Pro Asp Pro Gly Leu Pro Val Pro Pro Ala Leu Cys Gly Asn
134              410             415             420
136  ggc ttc gtg gaa gcg ggc gag gag tgt gac tgc ggc cct ggc cag gag   1350
137  Gly Phe Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Pro Gly Gln Glu
138          425             430             435
140  tgc cgc gac ctc tgc tgc ttt gct cac aac tgc tcg ctg cgc ccg ggg   1398
141  Cys Arg Asp Leu Cys Cys Phe Ala His Asn Cys Ser Leu Arg Pro Gly
142      440             445             450
144  gcc cag tgc gcc cac ggg gac tgc tgc gtg cgc tgc ctg ctg aag ccg   1446
145  Ala Gln Cys Ala His Gly Asp Cys Cys Val Arg Cys Leu Leu Lys Pro
146  455             460             465             470
148  gct gga gcg ctg tgc cgc cag gcc atg ggt gac tgt gac ctc cct gag   1494
149  Ala Gly Ala Leu Cys Arg Gln Ala Met Gly Asp Cys Asp Leu Pro Glu
150              475             480             485
152  ttt tgc acg ggc acc tcc tcc cac tgt ccc cca gac gtt tac cta ctg   1542
153  Phe Cys Thr Gly Thr Ser Ser His Cys Pro Pro Asp Val Tyr Leu Leu
154              490             495             500
156  gac ggc tca ccc tgt gcc agg ggc agt ggc tac tgc tgg gat ggc gca   1590
157  Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly Tyr Cys Trp Asp Gly Ala
158              505             510             515
160  tgt ccc acg ctg gag cag cag tgc cag cag ctc tgg ggg cct ggc tcc   1638
161  Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln Leu Trp Gly Pro Gly Ser
162      520             525             530
164  cac cca gct ccc gag gcc tgt ttc cag gtg gtg aac tct gcg gga gat   1686
165  His Pro Ala Pro Glu Ala Cys Phe Gln Val Val Asn Ser Ala Gly Asp
166  535             540             545             550
168  gct cat gga aac tgc ggc cag gac agc gag ggc cac ttc ctg ccc tgt   1734
169  Ala His Gly Asn Cys Gly Gln Asp Ser Glu Gly His Phe Leu Pro Cys
170              555             560             565
172  gca ggg agg gat gcc ctg tgt ggg aag ctg cag tgc cag ggt gga aag   1782
173  Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu Gln Cys Gln Gly Gly Lys
174              570             575             580
176  ccc agc ctg ctc gca ccg cac atg gtg cca gtg gac tct acc gtt cac   1830
177  Pro Ser Leu Leu Ala Pro His Met Val Pro Val Asp Ser Thr Val His
178          585             590             595
180  cta gat ggc cag gaa gtg act tgt cgg gga gcc ttg gca ctc ccc agt   1878
181  Leu Asp Gly Gln Glu Val Thr Cys Arg Gly Ala Leu Ala Leu Pro Ser
182          600             605             610
184  gcc cag ctg gac ctg ctt ggc ctg ggc ctg gta gag cca ggc acc cag   1926
185  Ala Gln Leu Asp Leu Leu Gly Leu Gly Leu Val Glu Pro Gly Thr Gln
186  615             620             625             630
188  tgt gga cct aga atg gtg tgc cag agc agg cgc tgc agg aag aat gcc   1974
189  Cys Gly Pro Arg Met Val Cys Gln Ser Arg Arg Cys Arg Lys Asn Ala
190              635             640             645
192  ttc cag gag ctt cag cgc tgc ctg act gcc tgc cac agc cac ggg gct   2022
193  Phe Gln Glu Leu Gln Arg Cys Leu Thr Ala Cys His Ser His Gly Ala
194              650             655             660
196  ggg ctc cac cct tct gtg aca agc cag gct ttg gtg gca gca tgg aca   2070
197  Gly Leu His Pro Ser Val Thr Ser Gln Ala Leu Val Ala Ala Trp Thr
```

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```
198        665          -          670                    675
200   gtg gcc ctg tgc agg ctg aaa acc atg aca cct tcc tgc tgg cca tgc        2118
201   Val Ala Leu Cys Arg Leu Lys Thr Met Thr Pro Ser Cys Trp Pro Cys
202        680                    685                    690
204   tcc tca gcg tcc tgc tgc ctc tgc tcc cag ggg ccg gcc tgg cct ggt        2166
205   Ser Ser Ala Ser Cys Cys Leu Cys Ser Gln Gly Pro Ala Trp Pro Gly
206   695                    700                    705                710
208   gtt gct acc gac tcc cag gag ccc atc tgc agc gat gca gct ggg gct        2214
209   Val Ala Thr Asp Ser Gln Glu Pro Ile Cys Ser Asp Ala Ala Gly Ala
210                    715                    720                    725
213   gca gaa ggg acc ctg cgt gca gtg gcc cca aag atg gcc cac aca ggg        2262
214   Ala Glu Gly Thr Leu Arg Ala Val Ala Pro Lys Met Ala His Thr Gly
215                    730                    735                    740
217   acc acc ccc tgg gcg gcg ttc acc cca tgg agt tgg gcc cca cag cca        2310
218   Thr Thr Pro Trp Ala Ala Phe Thr Pro Trp Ser Trp Ala Pro Gln Pro
219             745                    750                    755
221   ctg gac agc cct ggc ccc tgg acc ctg aga act ctc atg agc cca gca        2358
222   Leu Asp Ser Pro Gly Pro Trp Thr Leu Arg Thr Leu Met Ser Pro Ala
223        760                    765                    770
225   gcc acc ctg aga agc ctc tgc cag cag tct cgc ctg acc ccc aag atc        2406
226   Ala Thr Leu Arg Ser Leu Cys Gln Gln Ser Arg Leu Thr Pro Lys Ile
227   775                    780                    785                790
229   aag tcc aga tgc caa gat cct gcc tct ggt gag agg tagctcctaa             2452
230   Lys Ser Arg Cys Gln Asp Pro Ala Ser Gly Glu Arg
231                    795                    800
233   aatgaacaga tttaaagaca ggtggccact gacagccact ccaggaactt gaactgcagg      2512
234   ggcagagcca gtgaatcacc ggacctccag cacctgcagg cagcttggaa gtttcttccc      2572
235   cgagtggagc ttcgacccac ccactccagg aacccagagc cacattagaa gttcctgagg      2632
236   gctggagaac actgctgggc acactctcca gctcaataaa ccatcagtcc cagaagcaaa      2692
237   ggtcacacag cccctgacct ccctcaccag tggaggctgg gtagtgctgg ccatcccaaa      2752
238   agggctctgt cctgggagtc tggtgtgtct cctacatgca atttccacgg acccagctct      2812
239   gtggagggca tgactgctgg ccagaagcta gtggtcctgg ggccctatgg ttcgactgag      2872
240   tccacactcc cctggagcct ggctggcctc tgcaaacaaa cataattttg gggaccttcc      2932
241   ttcctgtttc ttcccaccct gtcttctccc ctaggtggtt cctgagcccc cacccccaat      2992
242   cccagtgcta cacctgaggt tctggagctc agaatctgac agcctctccc ccattctgtg      3052
243   tgtgtcgggg ggacagaggg aaccatttaa gaaaagatac caaagtagaa gtcaaaagaa      3112
244   agacatgttg gctataggcg tggtggctca tgcctataat cccagcactt tgggaagccg      3172
245   gggtaggagg atcaccagag gccagcaggt ccacaccagc ctgggcaaca cagcaagaca      3232
246   ccgcatctac agaaaaattt taaaattagc tgggcgtggt ggtgtgtacc tgtaggccta      3292
247   gctgctcagg aggctgaagc aggaggatca cttgagcctg agttcaacac tgcagtgagc      3352
248   tatggtggca ccactgcact ccagcctggg tgacagagca agaccctgtc tctaaaataa      3412
249   attttaaaaa gacatatta                                                   3431
251   <210> SEQ ID NO: 2
252   <211> LENGTH: 802
253   <212> TYPE: PRT
254   <213> ORGANISM: Homo sapiens
256   <400> SEQUENCE: 2
257   Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
258   1               5                   10                  15
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```
259  Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
260          20              25              30
261  Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
262          35                  40              45
263  Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
264      50                  55              60
265  Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
266  65              70              75              80
267  Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
268              85              90              95
269  Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
270          100             105             110
271  His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
272          115             120             125
273  Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
274      130             135             140
275  Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
276  145             150             155             160
277  Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
278              165             170             175
279  Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
280          180             185             190
281  Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
282          195             200             205
283  Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
284      210             215             220
285  Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
286  225             230             235             240
287  Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
288              245             250             255
289  Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr
290          260             265             270
291  Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly
292          275             280             285
293  Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg
294      290             295             300
295  Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys
296  305             310             315             320
297  Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro
298              325             330             335
299  Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly
300          340             345             350
301  Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Ala Glu Ser
302          355             360             365
303  Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val
304      370             375             380
305  Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly
306  385             390             395             400
307  Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro
```

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

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L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6